

Figure 1A
Neutrokine-α

1 AAATTCAGGATAACTCTCCTGAGGGGTGAGCCCAAGCCCTGCCATGTAGTGCACGCAGGAC 60

61 ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGIGGTCACCTATTCTAAAGGCC 120

121 CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC 180
1 M D D S T E R E Q S R L 12

181 TTACTTCTTGCCCTTAAGAAAAGAGAAGAAATGAACTGAAGGAGTGTGTTTCCATCCTCC 240
13 T S C L K K R E E M K L K E C V S I L P 32
CD-I

241 CACGGAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCT 300
33 R K E S P S V R S S K D G K L L A A T L 52
CD-I

301 TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTCTACCAGGTGGCCGCC 360
53 L L A L L S C C L T V V S F Y Q V A A L 72

361 TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC 420
73 Q G D L A S L R A E L Q G H H A E K L P 92
CD-II

421 CAGCAGGAGCAGGAGCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGAC 480
93 A G A G A P K A G L E E A P A V T A G L 112
CD-III

481 TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA 540
113 K I F E P P A P G E G N S S Q N S R N K 132

541 AGCGTGCCGTTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAG 600
133 R A V Q G P E E T V T Q D C L Q L I A D 152
CD-IV

601 ACAGTGAACACCAACTATACAAAAAGGATCTTACACATTGTTCATGGCTTCTCAGCT 660
153 S E T P T I Q K G S Y T F V P W L L S F 172
CD-V

661 TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTT 720
173 K R G S A L E E K E N K I L V K E T G Y 192
CD-V CD-VI

721 ACTTTTATATATATGGTCAGGTTTATATACTGATAAGACCTACGCCATGGGACATCTAA 780
193 F F I Y G Q V L Y T D K T Y A M G H L I 212
CD-VI CD-VII

781 TTCAGAGGAAGAAGTCCATGTCTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT 840
213 Q R K K V H V F G D E L S L V T L F R C 232
CD-VII CD-VIII

841 GTATTCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTTCAGCTGGCATTGCAA 900
233 I Q N M P E T L P N N S C Y S A G I A K 252
CD-VIII CD-IX

Figure 1B
Neutrokin-α

901	AACTGGAAGAAGGAGATGAACTCCAACCTTGCATACCAAGAGAAAATGCACAAATATCAC	960
253	<u>L E E G D E L Q L A I P R E N A Q I S L</u>	272
	CD-X	
961	TGGATGGAGATGTCACATTTTTTGGTGCATTGAAACTGCTGTGACCTACTTACACCATGT	1020
273	<u>D G D V T F F G A L K L L</u>	285
	CD-XI	
1021	CTGTAGCTATTTTCTCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA	1080
1081	CCAAAAAAAAAAAAAAAAAAAA 1100	



	10	20	30	
1	M S T E S M I R D V E L	- - - - -	- - - - -	A E E A TNFalpha
1	M - - - - -	- - - - -	- - - - -	T P P E R L TNFbeta
1	M G A - - - - -	- - - - -	- - - - -	- - - - - LTbeta
1	M Q Q P F N Y P Y P Q I Y W - V D S S A S S P W A P P G T V			FasLigand
1	M D D S T E R E Q S R L	T S C L K K K R E E M K L	K E C V S I	Neutrokin alpha
1	M D D S T E R E Q S R L	T S C L K K K R E E M K L	K E C V S I	Neutrokin alphaSV
	40	50	60	
17	L P K K T	G G P Q - - G S R R - - - - -	- - - - -	TNFalpha
8	F - - - - -	- - - - -	- - - - -	TNFbeta
4	- - - - L G L E G R G G - - - - -	- - - - -	- - - - -	LTbeta
30	L P C P T S V P R R P G Q R R P P P P P P P P L P P P P P			FasLigand
31	L P R K E S P S V R S S K D - - - G K L L A A T L L L A L L			Neutrokin alpha
31	L P R K E S P S V R S S K D - - - G K L L A A T L L L A L L			Neutrokin alphaSV
	70	80	90	
30	- - - - -	- - - - -	- - - - C L F L S L F S	TNFalpha
9	- - - - - L P R V R G T T L H L L L L G L L L V L L P			TNFbeta
12	- - - - - - R L Q G R G S L L A V A G A T S L V T			LTbeta
60	P P P L P P L P L P L P L K K R G N H S T G L C L L V M F F M			FasLigand
58	S C C L T V V S F Y Q V A A L Q G D L A S L R A E L Q G H H			Neutrokin alpha
58	S C C L T V V S F Y Q V A A L Q G D L A S L R A E L Q G H H			Neutrokin alphaSV
	100	110	120	
38	F L - - I V A G A T T L F C L L H F G V I G P Q R E E F P R			TNFalpha
31	G A Q G L P G V G L - - - - -	- - - - -	- - - - -	TNFbeta
32	L L L A V P I T V L A V L A L V P Q D Q G G L V T E T A D P			LTbeta
90	V L V A L V G L G L G M F Q L F H L Q K E L A E L R E S T S			FasLigand
88	A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P			Neutrokin alpha
88	A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P			Neutrokin alphaSV
	130	140	150	
66	D L S L I S - P L A - Q A V R S S S R T P S D - - - K P V A			TNFalpha
41	- - - T P S - A A Q - T A R Q H P K M H L A H S T L K P A A			TNFbeta
62	G A Q A Q Q - G L G F Q K L P E E E P E T D L S P G L P A A			LTbeta
120	Q M H T A S - S L E - K Q I G H P S P P P E K K E L R K V A			FasLigand
118	P A P G E G N S S Q N S R N K R A V Q G P E E T V T Q D C L			Neutrokin alpha
118	P A P G E G N S S Q N S R N K R A V Q G P E E T - - - - -			Neutrokin alphaSV
	160	170	180	
91	H V V A N P Q A E G - Q - - - - - L Q W L N R R A N A L L			TNFalpha
66	H L I G D P S K Q N - S - - - - - L L W R A N T D R A F L			TNFbeta
91	H L I G A P L K - G Q G - - - - - L G W E T T K E Q A F L			LTbeta
148	H L T G K S N S R S M P - - - - - L E W E D T Y G I V L L			FasLigand
148	Q L I A D S E T P T I Q K G S Y T F V P W L - - - - L S F K			Neutrokin alpha
142	- - - - - - - - - - - G S Y T F V P W L - - - - L S F K			Neutrokin alphaSV

	190	200	210	
114	A N G V E L R D N - Q L V V P S E G L Y L I Y S Q V L F K G	TNFalpha		
89	Q D G F S L S N N - S L L V P T S G I Y F V Y S Q V V F S G	TNFbeta		
114	T S G T Q F S D A E G L A L P Q D G L Y Y L Y C L V G Y R G	L1beta		
172	- S G V K Y K K G - G L V I N E T G L Y F V Y S K V Y F R G	FasLigand		
174	R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D	Neutrokin alpha		
155	R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D	Neutrokin alphaSV		
	220	230	240	
143	Q G C P - - - - S T H V L L T H T I S R I A V S Y Q T K	TNFalpha		
118	K A Y S P - - K A T S S P L Y L A H E V Q L F S S Q Y P F H	TNFbeta		
144	R A P P G G G D P Q G R S V T L R S S L Y R A G G A Y G P G	L1beta		
200	Q S C N - - - - - N L P L S H K V Y M R N S K Y P Q D	FasLigand		
204	K T Y A M G - - - - - H L I Q R K K V H V F G D E L S - -	Neutrokin alpha		
185	K T Y A M G - - - - - H L I Q R K K V H V F G D E L S - -	Neutrokin alphaSV		
	250	260	270	
167	V N - - L L S A I K S P C Q R E T P E - - G A E A K P W Y E	TNFalpha		
146	V P - - L L S S Q K M V Y P - - - - - G L Q E P W L H	TNFbeta		
174	T P E L L L E G A E T V T P V L D P A R R Q G Y G P L W Y T	L1beta		
222	L V - - M M E G K M M S Y C - - - - - T T G Q M W A R	FasLigand		
226	L V T L F R C I Q N M P E T L P N - - - - - - - - - N	Neutrokin alpha		
207	L V T L F R C I Q N M P E T L P N - - - - - - - - - N	Neutrokin alphaSV		
	280	290	300	
193	P I Y L G G V F Q L E K G D R L S A E I N R P D Y L D F A E	TNFalpha		
166	S M Y H G A A F Q L T Q G D Q L S T H T D G I P H L V L S P	TNFbeta		
204	S V G F G G L V Q L R R G E R V Y V N I S H P D M V D F A R	L1beta		
242	S S Y L G A V F N L T S A D H L Y V N V S E L S L V N F E E	FasLigand		
244	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D	Neutrokin alpha		
225	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D	Neutrokin alphaSV		
	310			
223	S G Q V Y F G I I A L	TNFalpha		
196	S - T V F F G A F A L	TNFbeta		
234	- G K T F F G A V M V G	L1beta		
272	S - Q T F F G L Y K L	FasLigand		
274	G D V T F F G A L K L L	Neutrokin alpha		
255	G D V T F F G A L K L L	Neutrokin alphaSV		

Figure 3
Neutrokin- α

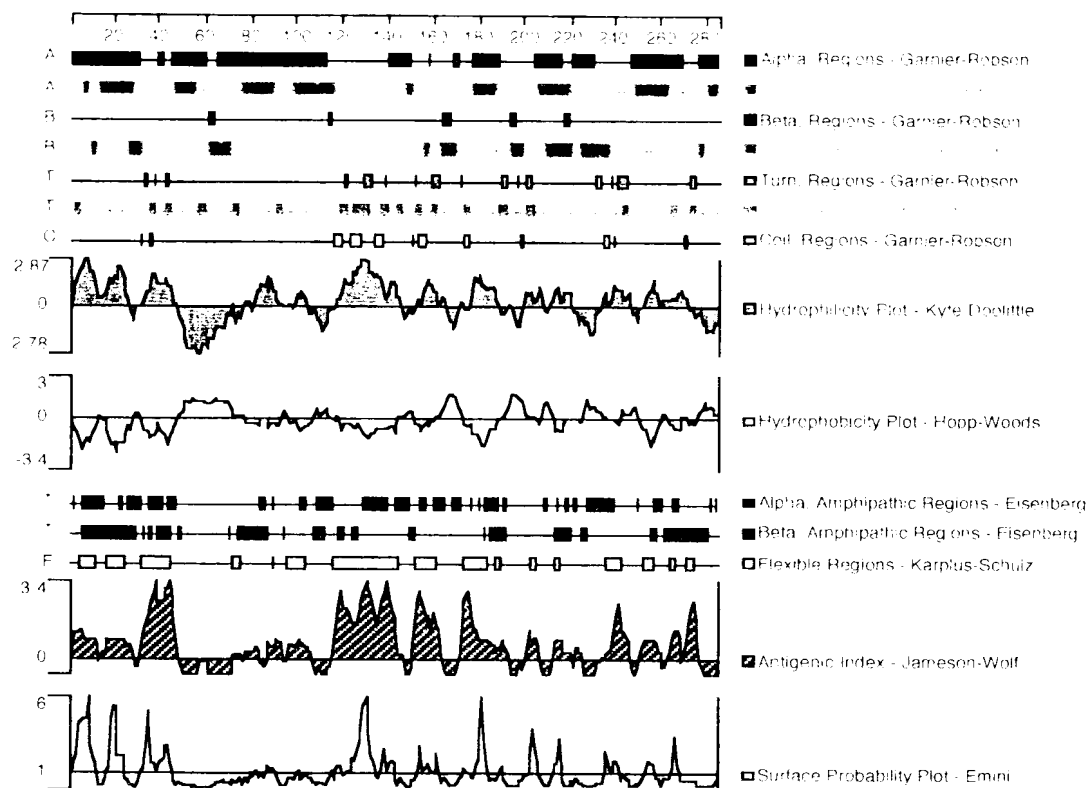


FIGURE 4 A

	1		50
HSOAD55RA	GGNTAACTCT CCTGAGGGGT	GAGCCAAGCC CTGCCATGTA
HNEDU15X	...AAATTCA	GGATAACTCT CCTGAGGGGT	GAGCCAAGCC CTGCCATGTA
HSLAH84R	.AATTCGGCA	NAGNAACTG GTTACTTTT	TATATATGGT CAGGTTTAT
HLTBM08R	AATTCGGCAC	GAGCAAGGCC GGCCTGGAGG	AAGCTCCAGC TGTCACCGCG
	51		100
HSOAD55R	GTGCACGCAG	GACATCANCA A..ACACANN	NNNCAGGAAA TAATCCATTC
HNEDU15X	GTGCACGCAG	GACATCAACA A..ACACAGA	TAACAGGAAA TGATCCATTC
HSLAH84R	ATACTGATAA	GACCTACGCC ATGGGACATC	TAGTTCAGAG GAAGAAGGTC
HLTBM08R	GGACTGAAAA	TCTTTGAACC ACCAGCTCCA	GGAGAAGGCA ACTCCAGTCA
	101		150
HSOAD55R	CCTGTGGTCA	CTTATTCTAA AGGCCCAAC	CTTCAAAGTT CAAGTAGTGA
HNEDU15X	CCTGTGGTCA	CTTATTCTAA AGGCCCAAC	CTTCAAAGTT CAAGTAGTGA
HSLAH84R	CATGTCTTTG	GGGATGAATT GAGTCTGGTG	ACTTTGTTTC GATGTATTCA
HLTBM08R	GAACAGCAGA	AATAAGCGTG CCGTTCAGGG	TCCAGAAGAA ACAGTCACTC
	151		200
HSOAD55R	TATGGATGAC	TCCACAGAAA GGGAGCAGTC	ACGCCTTACT TCTTGCCTTA
HNEDU15X	TATGGATGAC	TCCACAGAAA GGGAGCAGTC	ACGCCTTACT TCTTGCCTTA
HSLAH84R	AAATATGCCT	GAAACACTAC CCAATAATTC	CTGCTATTCA GCTGGCATTG
HLTBM08R	AAGACTGCTT	GCAACTGNNT GCAGACAGTG	AAACACCAAC TATACAAAAA
	201		250
HSOAD55R	AGAAAAGAGA	AGAAATGAAA CTGNAAGGAG	TGTGTTTCCA TCCTCCACG
HNEDU15X	AGAAAAGAGA	AGAAATGAAA CT.GAAGGAG	TGTGTTTCCA TCCTCCACG
HSLAH84R	CAAACTGGN	AGGAAGGA.. ...GATGAAC	TCCAACCTGC AATACCAGGG
HLTBM08R	GGCTCCCTTC	TGNTGCCACA TTTGGGCCAA	GGAATGGAGA GATTTCTTCG
	251		300
HSOAD55R	GAAGGAAAGC	CCCTCTNTCC GATCCTCCAA	AGACGGAAAG CTGCTGGCTG
HNEDU15X	GAAGGAAAGC	CCCTCTGTCC GATCCTCCAA	AGACGGAAAG CTGCTGGCTG
HSLAH84R	GAAAATGCAC	AATTATCACT GGGATGGAGA	TGTTACATT TTTTGGGTGC
HLTBM08R	TCTGGAAACA	TTTTGCCAAA CTCTTCAGAT	ACTCTTNCT CTCTGGGAAT
	301		350
HSOAD55R	CAACCTTGNT	GNTGGCATTG TGTTCTTGCT	GNCTCAAGGT GGTGTTNTT.
HNEDU15X	CAACCTTGCT	GCTGGCACTG CTGTCTTGCT	GCCTCACGGT GGTGTCTTTC
HSLAH84R	CATTGAACT	GCTGTGACCT NCTTACANCA	NGTGCTGTTN GCTATTTTNC
HLTBM08R	CAAAGGAAAA	TCTCTACTTA GATTNACACA	TTTGTTCCCA TGGGTNTCTT
	351		400
HSOAD55R
HNEDU15X	TACCAGGTGG	CCGCCCTGCA AGGGGACCTG	GCCAGCCTCC GGGCAGAGCT
HSLAH84R	CTNCCTNTTC	TNTGGTAACC TCTTAGGAAG	GAAGGATTCT TAACTGGGAA
HLTBM08R	AAGTTTTAAA	AGGGGAGTGC CTTAGGAGG	AAAAGGGGAT AAATATTGGC

FIGURE 4B

	401				450
HSOAD55R
HNEDU15X	GCAGGCGCCAC	CACGCGGAGA	AGCTGCCAGC	AGGAGCAGGA	GCCCCCAAGG
HSLAH84R	ATAACCCAAA	AAAANNTTAA	ANGGGTANGN	GNNANANGNG	GGGNNGTNN
HLTBM08R	CAAGGNACTG	GTTANTTTNT	AAATATGGTC	AGGTTTNTAT	ANCTGGTAGG
	451				500
HSOAD55R
HNEDU15X	CCGGCCCTGGA	GGAAGCTCCA	GCTGTCACCG	CGGGACTGAA	AATCTTTGAA
HSLAH84R	CNNGNNGNNT	TTTNGGNNTA	TNTTNTNNTN	GGGNNNGTA	AAAATGGGGC
HLTBM08R	CCTCGCCATG	GGCATTNATT	CANGGNGAGG	NCNNTCTTTT	GGGNTGA...
	501				550
HSOAD55R
HNEDU15X	CCACCAGCTC	CAGGAGAAGG	CAACTCCAGT	CAGAACAGCA	GAAATAAGCG
HSLAH84R	CNANGGGGGN	TTTTT.....
HLTBM08R
	551				600
HSOAD55R
HNEDU15X	TGCCGTTTTCAG	GGTCCAGAAG	AAACAGTCAC	TCAAGACTGC	TTGCAACTGA
HSLAH84R
HLTBM08R
	601				650
HSOAD55R
HNEDU15X	TTGCAGACAG	TGAAACACCA	ACTATACAAA	AAGGATCTTA	CACATTTGTT
HSLAH84R
HLTBM08R
	651				700
HSOAD55R
HNEDU15X	CCATGGCTTC	TCAGCTTTAA	AAGGGGAAGT	GCCCTAGAAG	AAAAAGAGAA
HSLAH84R
HLTBM08R
	701				750
HSOAD55R
HNEDU15X	TAAAAATATTG	GTCAAAGAAA	CTGGTTACTT	TTTTATATAT	GGTCAGGTTT
HSLAH84R
HLTBM08R
	751				800
HSOAD55R
HNEDU15X	TATATACTGA	TAAGACCTAC	GCCATGGGAC	ATCTAATTCA	GAGGAAGAAG
HSLAH84R
HLTBM08R

FIGURE 4C

	801		850
HSOAD55R
HNEDU15X	GTCCATGTCT	TTGGGGATGA	ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R
HLTBM08R
	851		900
HSOAD55R
HNEDU15X	TCAAAATATG	CCTGAAACAC	TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R
HLTBM08R
	901		950
HSOAD55R
HNEDU15X	TTGCAAAACT	GGAAGAAGGA	GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R
HLTBM08R
	951		1000
HSOAD55R
HNEDU15X	AATGCACAAA	TATCACTGGA	TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R
HLTBM08R
	1001		1050
HSOAD55R
HNEDU15X	ACTGCTGTGA	CCTACTTACA	CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R
HLTBM08R
	1051		1100
HSOAD55R
HNEDU15X	CTGTACCTCT	AAGAAGAAAG	AATCTAACTG AAAATACCAA AAAAAAAAAA
HSLAH84R
HLTBM08R
	1101		
HSOAD55R		
HNEDU15X	AAAAAA		
HSLAH84R		
HLTBM08R		

Figure 5A
Neutrokinine- α SV

1	ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCCTTACTTCTTCCCTTAAGAAAAGAGAA	50
1	M D D S T E R E Q S R L T S C L K K R E	20
61	GAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCACGGAAGGAAAGCCCTCTGTCCGA	120
21	E M K L K E C V S I L P R K E S P S V R	40
	CD-I	
121	TCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGTCTG	180
41	S S K D G K L L A A T L L L A L L S C C	60
	CD-I	
181	CTCAGGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG	240
61	L T V V S F Y Q V A A L Q G D L A S L R	80
	CD-II	
241	GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCAAGGCC	300
81	A E L Q G H H A E K L P A G A G A P K A	100
	CD-II	CD-III
301	GGCCTGGAGGAAGCTCCAGCTGTACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA	360
101	G L E E A P A V T A G L K I F E P P A P	120
	CD-III	
	#	
361	GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTTCAGGGTCCAGAAGAA	420
121	G E G N S S Q N S R N K R A V Q G P E E	140
421	ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA	480
141	T G S Y T F V P W L L S F K R G S A L E	160
	CD-IV	
481	GAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTTACTTTTTATATATGGTCAGGTT	540
161	E K E N K I L V K E T G Y F F I Y G Q V	180
	CD-IV	CD-V
541	TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTC	600
181	L Y T D K T Y A M G H L I Q R K K V H V	200
	CD-VI	CD-VII
601	TTTGGGGATGAATTGAGTCTGGTGACTTTGTTCGATGTATTCAAAATATGCCTGAAACA	660
201	F G D E L S L V T L F R C I Q N M P E T	220
	CD-VIII	CD-VIII
	#	
661	CTACCCCAATAATTCCTGCTATTTCAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACTC	720
221	L P N N S C Y S A G I A K L E E G D E L	240
	CD-IX	CD-X
721	CAACTTGCAATACCAAGAGAAAAATGCACAAATATCAGTGGATGGAGATGTCACATTTTTT	780
241	Q L A I P R E N A Q I S L D G D V T F F	260
	CD-X	CD-XI
781	GGTGCATTGAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTCTCCCTTTC	840
261	G A L K L L	266
	CD-XI	

Figure 5B
Neutrokinine- α SV

841 TCCTGTAACCTCTAAGAAGAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAAAAA 900
901 AAA 903

Figure 6
Neutrokin-αSV

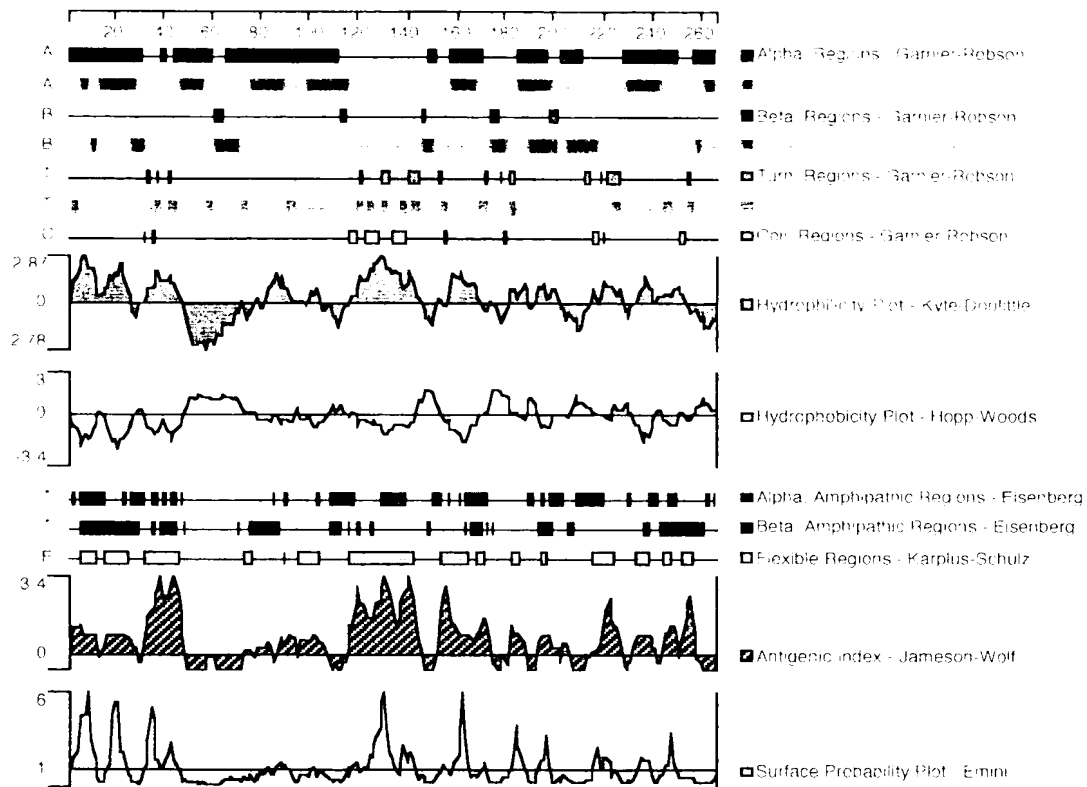


Figure 7

a.

leutokine-
alpha MDDSTEREQSRLTSC LKKREEMKLKECVSILPRKESPSVRS 41

Transmembrane Region

SKD G K L L A A T L L L A L L S C C L T V V S F Y Q V A A L Q G D L A S L R A E 82

LQGHHA EK L P A G A G A P K A G L E E A P A V T A G L K I F E P P A P G E G 123

↓

NSSQNSRNRKRAVQGP EETVT A QDCLQLIADSETPTIQKGSYT 164

April HSV L H L V P I N A T S K - D D S D V T 134

TNF K P V A H V V A N P Q A E G Q - - - - - 102

LT α K P A A H L I G D P S K Q N S - - - - - 77

A' B' B C

FVPWLLS - - - - - F K R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L 200

EVMWQPA - - - - - L R R G R G L Q A Q G Y G V R I Q D A G V Y L L Y S Q V L 170

-LQWLNRRRANALLANGVELRD - - N Q L V V P S E G L Y L I Y S Q V L 139

-LLWRANTDRAFLQDGFSLSN - - N S L L V P T S G I Y F V Y S Q V V 114

D E

YTDKTY - - - - - A M G H L I Q R K K V H V F G D E L S L V T L F R C I Q N M P 237

FQDVTF - - - - - T M G Q V V S R E - - - - - G Q G R Q E T L F R C I R S M P 201

FKGQGCP - - - - - S T H V L L T H T I S R I A V S Y Q T K V N L L S A I K S P 176

FSGKAYS PKATSSPLYLAHEVQLFSSQYPFHVPL LSSQKMV 155

F G

E - - T L P - - - - - - N N S C Y S A G I A K L E E G D E L Q L A I P R E N A 268

SHPDRA - - - - - - Y N S C Y S A G V F H L H Q G D I L S V I I P R A R A 234

CQRETPEGAEAKPWYEPIYLGGVFQLEK GDRLSAEINRPDY 217

YP - - - - - G L Q E P W L H S M Y H G A A F Q L T Q G D Q L S T H T D G I P H 190

H

QISLDGDVTFFGALKLL 285

KLNLSPHGTFLGFVKL 250

LDFAESGQVYFGIIAL 233

LVLS - P S T V F F G A F A L 205

b.

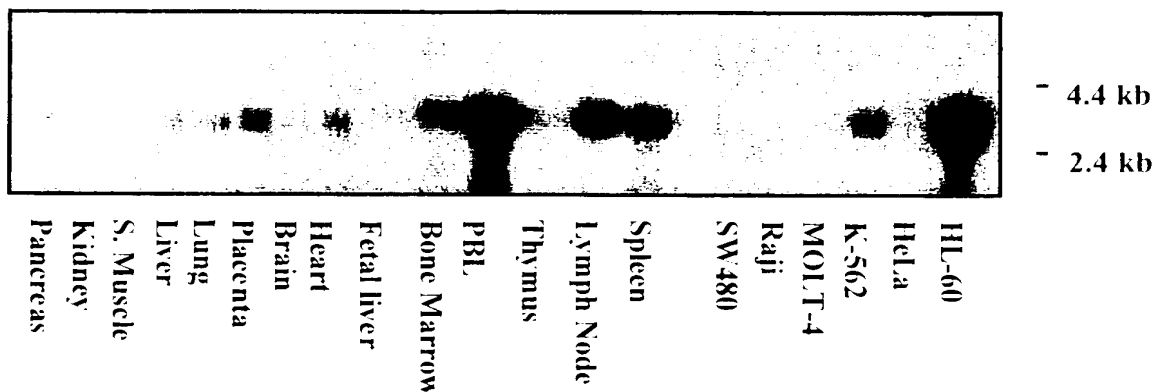
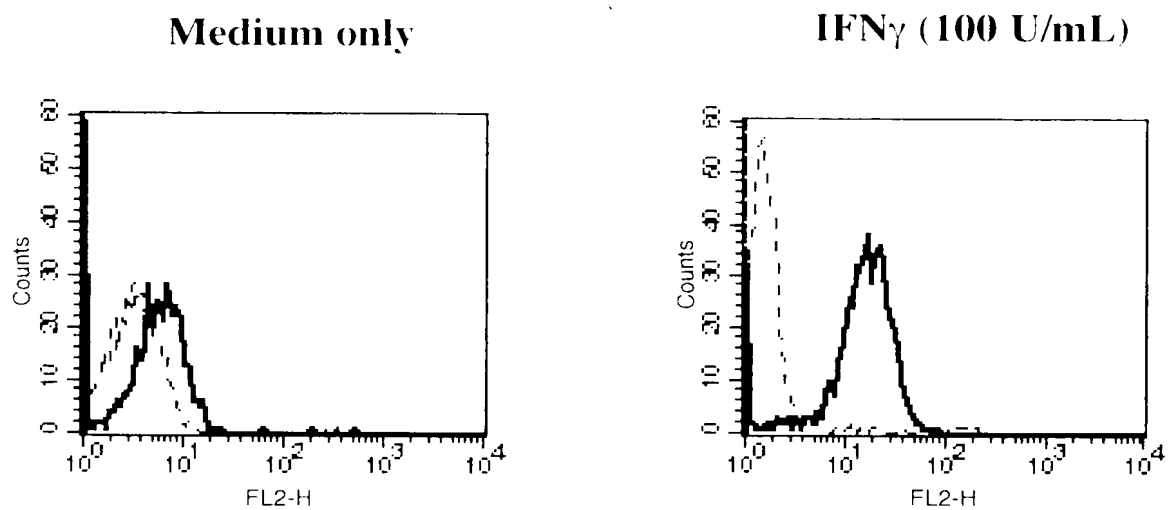


Figure 8

a.



b.

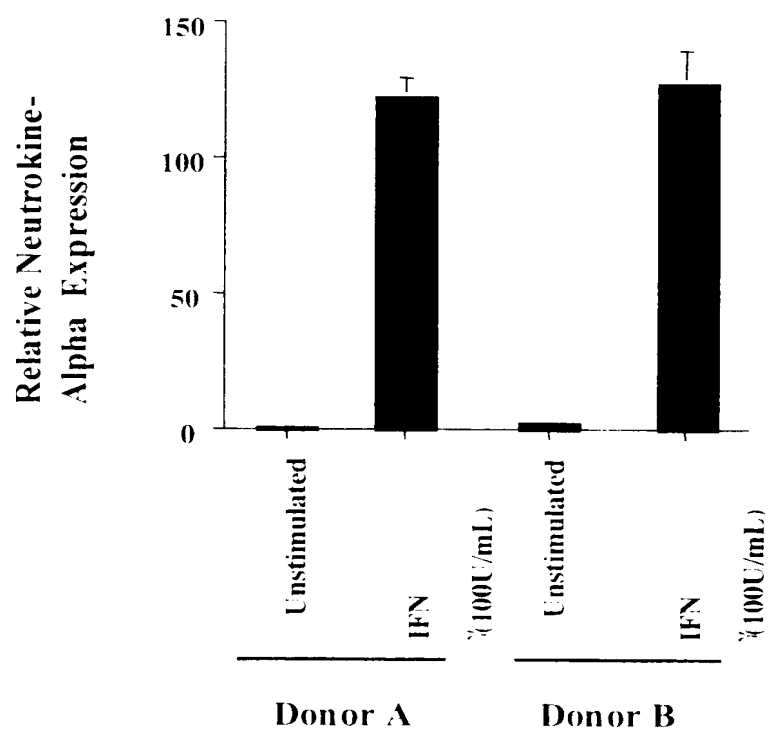
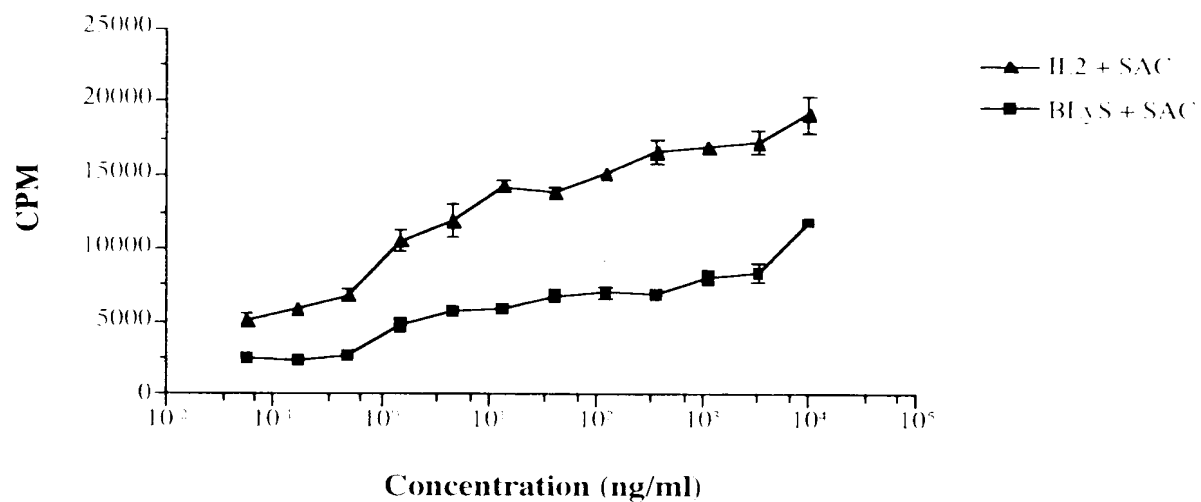


Figure 9

a.



b.

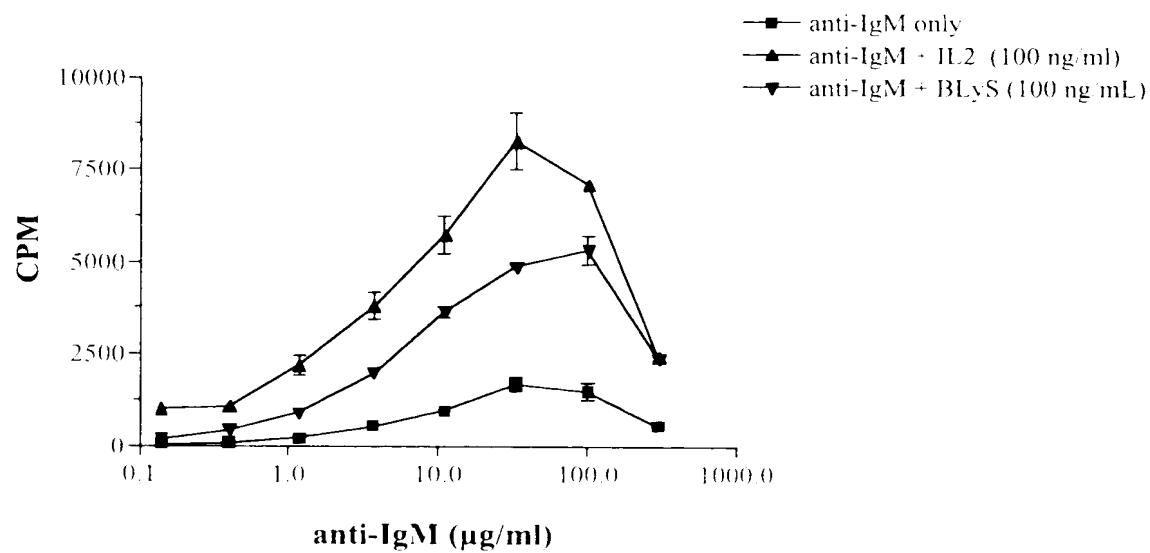


Figure 10

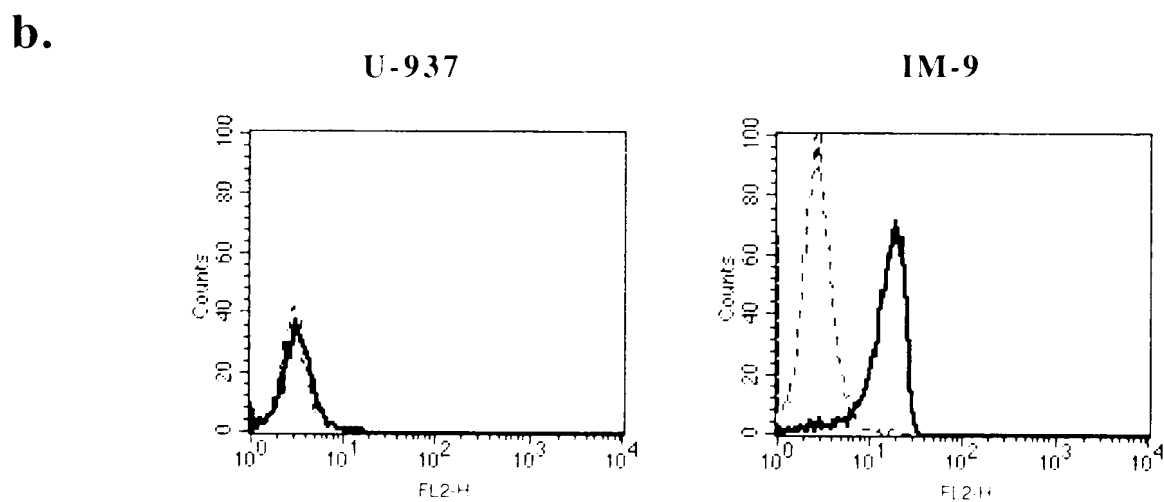
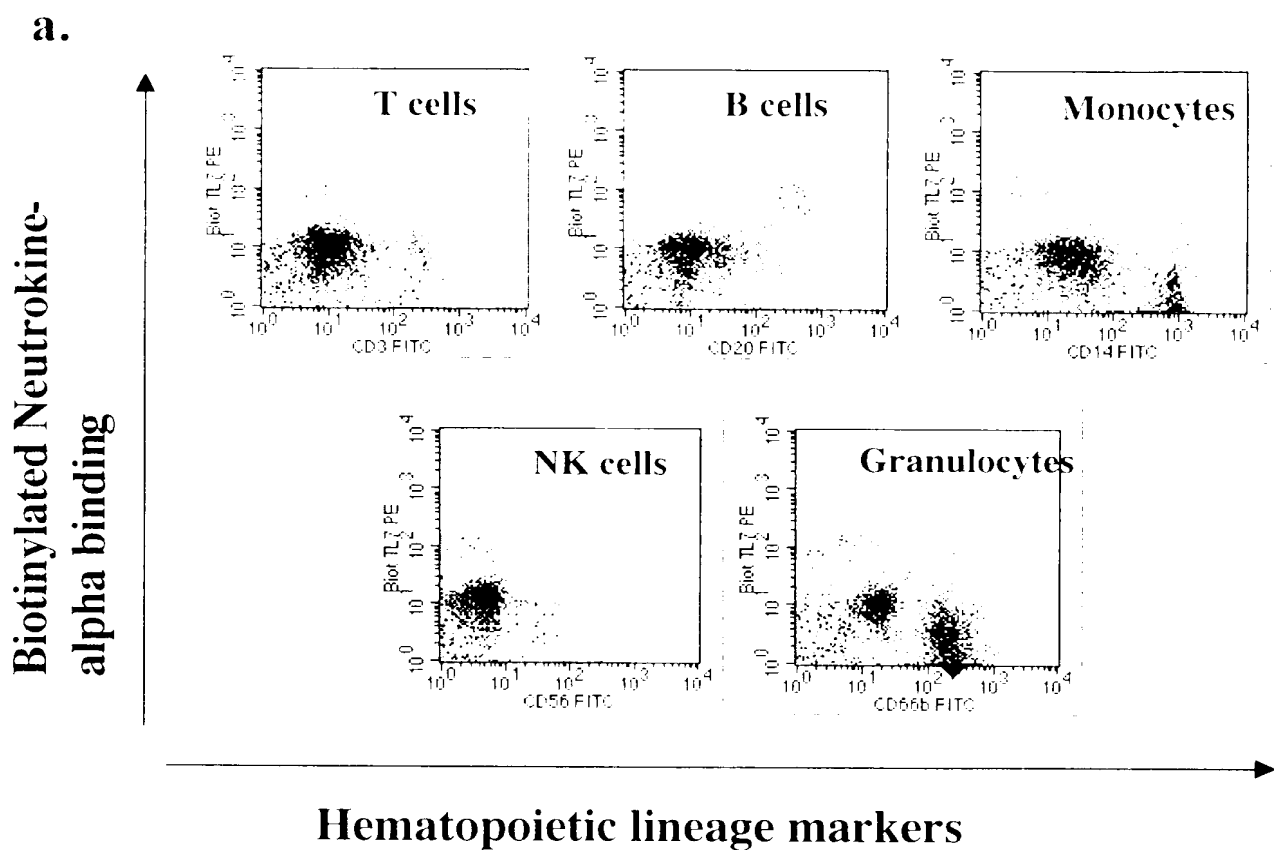


Figure 11

